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PTO/SB/21 (08-00)

Approved for use through 10/31/2002. OMB 0651-0031

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TRANSMITTAL FORM

(to be used for all correspondence after initial filing)

Application Number	09/597,796
Filing Date	June 20, 2000
First Named Inventor	Skeiky, Yasir
Group Art Unit	1645
Examiner Name	Swartz, Rodney P.
Attorney Docket Number	014058-009050US

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39

ENCLOSURES (check all that apply)

<input type="checkbox"/> Fee Transmittal Form <input type="checkbox"/> Fee Attached <input type="checkbox"/> Amendment / Reply <input type="checkbox"/> After Final <input type="checkbox"/> Affidavits/declaration(s) <input type="checkbox"/> Extension of Time Request <input type="checkbox"/> Express Abandonment Request <input type="checkbox"/> Information Disclosure Statement <input type="checkbox"/> Certified Copy of Priority Document(s) <input type="checkbox"/> Response to Missing Parts/ Incomplete Application <input type="checkbox"/> Response to Missing Parts under 37 CFR 1.52 or 1.53	<input type="checkbox"/> Assignment Papers (for an Application) <input type="checkbox"/> Drawing(s) <input type="checkbox"/> Licensing-related Papers <input type="checkbox"/> Petition <input type="checkbox"/> Petition to Convert to a Provisional Application <input type="checkbox"/> Power of Attorney, Revocation Change of Correspondence Address <input type="checkbox"/> Terminal Disclaimer <input type="checkbox"/> Request for Refund <input type="checkbox"/> CD, Number of CD(s)	<input type="checkbox"/> After Allowance Communication to Group <input type="checkbox"/> Appeal Communication to Board of Appeals and Interferences <input type="checkbox"/> Appeal Communication to Group (Appeal Notice, Brief, Reply Brief) <input type="checkbox"/> Proprietary Information <input type="checkbox"/> Status Letter <input checked="" type="checkbox"/> Other Enclosure(s) (please identify below): Return Postcard; Communication Under 37 CFR 1.821-1.825 and Amendment; disk containing sequence listing; copy of Notice to Comply..
Remarks		The Commissioner is authorized to charge any additional fees to Deposit Account 20-1430.

SIGNATURE OF APPLICANT, ATTORNEY, OR AGENT

Firm and Individual name	Townsend and Townsend and Crew LLP Annette S. Parent	Reg. No. 42,058
Signature		
Date	December 4, 2002	

CERTIFICATE OF MAILING

I hereby certify that this correspondence is being deposited with the United States Postal Service with sufficient postage as first class mail in an envelope addressed to: Commissioner for Patents, Washington, D.C. 20231 on this date:

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P.O. Box 2327, Arlington, VA 22202 on this date

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SF 1412252 v1



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ASP/UA

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/597,796	06/20/2000	Yasir Skeiky	014058-009050US	6269

20350 7590 11/04/2002

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EIGHTH FLOOR
SAN FRANCISCO, CA 94111-3834

EXAMINER

SWARTZ, RODNEY P

ART UNIT	PAPER NUMBER
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1645

DATE MAILED: 11/04/2002

15

Response Due SCR. LIST. 12/4/02 ALB

Please find below and/or attached an Office communication concerning this application or proceeding.



UNITED STATES DEPARTMENT OF COMMERCE
Patent and Trademark Office
COMMISSIONER OF PATENTS AND TRADEMARKS
Washington, D.C. 20231

SERIAL NUMBER	FILING DATE	FIRST NAMED APPLICANT	ATTORNEY DOCKET NO.
09/597,796			

EXAMINER	
Rodney P. Swartz, Ph.D.	
ART UNIT	PAPER NUMBER
1645	

DATE MAILED:

Please find below a communication from the EXAMINER in charge of this application
Commissioner of Patents

This Application contains sequence disclosures that are encompassed by the definitions for nucleotide and/or amino acid sequences set forth in 37 C.F.R. § 1.821(a)(1) and (a)(2). However, this application fails to comply with the requirements of 37 CFR §§ 1.821 - 1.825 for the reason(s) set forth on the attached Notice To Comply With Requirements For Patent Applications Containing Nucleotide Sequences And/Or Amino Acid Sequence Disclosures.

Any inquiry concerning this communication should be directed to Examiner Rodney P. Swartz, Ph.D., Art Unit 1645, whose telephone number is (703) 308-4244. If unable to reach the examiner, Lynette Smith, SPE, can be contacted at (703) 308-3909.

Any questions regarding compliance with the sequence rules requirements specifically should be directed to the departments listed at the bottom of the Notice To Comply.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

APPLICANT IS GIVEN ONE MONTH FROM THE DATE OF THIS LETTER WITHIN WHICH TO COMPLY WITH THE SEQUENCE RULES, 37 C.F.R. §§ 1.821 - 1.825. Failure to comply with these requirements will result in ABANDONMENT of the application under 37 C.F.R. § 1.821(g). Extensions of time may be obtained by filing a petition accompanied by the extension fee under the provisions of 37 C.F.R. § 1.136. In no case may an applicant extend the period for response beyond the six month statutory period. Direct the response to the undersigned. Applicant is requested to return a copy of the attached Notice to Comply with the response.

Rodney P. Swartz, Ph.D.
November 4, 2002



Application No. 09/597,796

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CAR §1.821 - §1.825 for the following reasons(s):

- ☒ 1. This application clearly fails to comply with the requirements of 37 CAR §1.821 - §1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990, and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CAR §1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CAR §1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CAR §1.822 and/or §1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing".
- ☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CAR §1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CAR §1.821(e).
- ☐ 7. Other: _____

APPLICANT MUST PROVIDE:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".
- ☒ An initial or substitute paper copy of the "Sequence Listing", as were as an amendment directing its entry into the specification.
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CAR §1.821(e) or §1.821(f) or §1.821(g) or §1.825(b) or §1.825(d).

FOR QUESTIONS REGARDING COMPLIANCE WITH THESE REQUIREMENTS, PLEASE CONTACT:

For Rules Interpretation, call (703) 308-1123
For CRF Submission help, call (703)308-4212
For Patentin Software help, call (703) 557-0400

PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE.

ERROR DETECTED**SUGGESTED CORRECTION**SERIAL NUMBER: 09/597,796B

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO S

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading).
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X°(insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220>
Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

1600

RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/09/597,796B

TIME: 12:32:10

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Output Set: N:\CRF3\01152002\I597796B.raw

Does Not Comply
Corrected Diskette Needed

PP 3, 6-8

3 <110> APPLICANT: Skeiky, Yasir
 4 Reed, Steven
 5 Alderson, Mark
 6 Corixa Corporation
 8 <120> TITLE OF INVENTION: Fusion Proteins of Mycobacterium Tuberculosis
 10 <130> FILE REFERENCE: 014058-009050US
 12 <140> CURRENT APPLICATION NUMBER: US 09/597,796B
 13 <141> CURRENT FILING DATE: 2001-06-20
 15 <150> PRIOR APPLICATION NUMBER: US 09/056,556
 16 <151> PRIOR FILING DATE: 1998-04-07
 18 <150> PRIOR APPLICATION NUMBER: US 09/223,040
 19 <151> PRIOR FILING DATE: 1998-12-30
 21 <150> PRIOR APPLICATION NUMBER: WO PCT/US99/07717
 22 <151> PRIOR FILING DATE: 1999-04-07
 24 <150> PRIOR APPLICATION NUMBER: US 09/287,849
 25 <151> PRIOR FILING DATE: 1999-04-07
 27 <150> PRIOR APPLICATION NUMBER: US 60/158,338
 28 <151> PRIOR FILING DATE: 1999-10-07
 30 <150> PRIOR APPLICATION NUMBER: US 60/158,425
 31 <151> PRIOR FILING DATE: 1999-10-07
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 35 <170> SOFTWARE: PatentIn Ver. 2.1
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 38 <211> LENGTH: 588
 39 <212> TYPE: DNA
 40 <213> ORGANISM: Mycobacterium tuberculosis
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 43 <223> OTHER INFORMATION: Ra35, N-terminus of MTB32A (TbRa35FL)
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 46 <221> NAME/KEY: CDS
 47 <222> LOCATION: (1)..(588)
 48 <223> OTHER INFORMATION: Ra35
 50 <400> SEQUENCE: 1
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 63 <210> SEQ ID NO: 2
 64 <211> LENGTH: 195
 65 <212> TYPE: PRT
 66 <213> ORGANISM: Mycobacterium tuberculosis

RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/09/597,796B

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70 <400> SEQUENCE: 2

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 72 1 5 10 15
 73 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val Val
 74 20 25 30
 75 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 76 35 40 45
 77 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 78 50 55 60
 79 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 80 65 70 75 80
 81 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 82 85 90 95
 83 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 84 100 105 110
 85 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 86 115 120 125
 87 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 88 130 135 140
 89 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 90 145 150 155 160
 91 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
 92 165 170 175
 93 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
 94 180 185 190
 95 Ala Ala Ser
 96 195

99 <210> SEQ ID NO: 3

100 <211> LENGTH: 1872

101 <212> TYPE: DNA

102 <213> ORGANISM: Mycobacterium tuberculosis

104 <220> FEATURE:

105 <223> OTHER INFORMATION: MTB32A (TbRa35FL) cDNA

107 <400> SEQUENCE: 3

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 110 gtcattggtg ctgagcgtgc tggctgccgt cgggctgggc ctggccacgg cgccggccca 180
 111 ggccggcccg ccggccttgt cgcaggaccg gttcgcgcac ttccccgcgc tgcccctcga 240
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 119 gacattgaac gggttgatcc agttcgatgc cgcaatccag cccggtgatt cgggcggggc 720
 120 cgtcgtcaac ggcctaggac aggtggctcg tatgaacacg gccgcgtccg ataacttcca 780
 121 gctgtcccg ggtgggcagg gattcgccat tccgatcggg caggcgatgg cgatcgcggg 840

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 123 cttgggtggt gtcgacaaca acggcaacgg cgcacgagtc caacgcgtgg tcggaagcgc 960
 124 tccggcgcca agtctcgga tctccaccgg cgacgtgatc accgcggtcg acggcgctcc 1020
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 128 cagcgtgat tgcgcgtga gccccgagt tccgtctccc gtgcgcgtgg cattgtggaa 1260
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 131 gatccgacct ggtttaagca cgcgctctc tacgaggtgc tggctccggc gttcttcgac 1440
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 133 tggcttgga tcgactgat ctgttgccgc cgttcctacg actcaccgct gcgcgacggc 1560
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 137 tacggtgact attacgtgtg gacgcacacc agcagcgct acaccgacgc ccggatcatc 1800
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 139 gcaccgattc tt 1872
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 143 <211> LENGTH: 355
 144 <212> TYPE: PRT
 145 <213> ORGANISM: Mycobacterium tuberculosis
 147 <220> FEATURE:
 148 <223> OTHER INFORMATION: MTB32A (TbRa35FL) protein
 150 <400> SEQUENCE: 4
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 152 1 5 10 15
 153 Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
 154 20 25 30
 155 Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 156 35 40 45
 157 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 158 50 55 60
 159 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 160 65 70 75 80
 161 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 162 85 90 95
 163 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 164 100 105 110
 165 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 166 115 120 125
 167 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 168 130 135 140
 169 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 170 145 150 155 160
 171 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 172 165 170 175
 173 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 174 180 185 190

see
 item 9
 on
 Error
 Summary
 Sheet

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176      195      200      205
177 Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
178      210      215      220
179 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
180 225      230      235      240
181 Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
182      245      250      255
183 Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
184      260      265      270
185 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
186      275      280      285
187 Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
188      290      295      300
189 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
190 305      310      315      320
191 Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
192      325      330      335
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194      340      345      350

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195 Pro Pro Ala

196 355

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200 <211> LENGTH: 447

201 <212> TYPE: DNA

202 <213> ORGANISM: Mycobacterium tuberculosis

204 <220> FEATURE:

205 <223> OTHER INFORMATION: MTBRa12 C-terminus of MTB32A (Ra35FL)

207 <400> SEQUENCE: 5

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210 caccgttcac atcgggccta ccgccttcct cggcttgggt gttgtcgaca acaacggcaa 180
211 cggcgacaga gtccaacgcg tggtcgggag cgctccggcg gcaagtctcg gcatctccac 240
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220 <212> TYPE: PRT

221 <213> ORGANISM: Mycobacterium tuberculosis

223 <220> FEATURE:

224 <223> OTHER INFORMATION: MTBRa12 C-terminus of MTB32A (Ra35FL)

226 <400> SEQUENCE: 6

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230      20      25      30
231 Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly

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RAW SEQUENCE LISTING

DATE: 01/15/2002

PATENT APPLICATION: US/09/597,796B

TIME: 12:32:10

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234          50          55          60
235 Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
236 65          70          75          80
237 Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
238          85          90          95
239 Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
240          100          105          110
241 Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
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243 Gly Pro Pro Ala
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247 <210> SEQ ID NO: 7
248 <211> LENGTH: 3058
249 <212> TYPE: DNA
250 <213> ORGANISM: Mycobacterium tuberculosis
252 <220> FEATURE:
253 <223> OTHER INFORMATION: MTB39 (TbH9) cDNA full-length
255 <400> SEQUENCE: 7
256 gatcgtagcc gtgcgagtgc tcgggcccgtt tgaggatgga gtgcacgtgt ctttcgtgat 60
257 ggcataccca gagatgttgg cggcgccggc tgacaccctg cagagcatcg gtgctaccac 120
258 tgtggctagc aatgccgctg cggcgccccc gacgactggg gtggtgcccc ccgctgccga 180
259 tgagggtgctg gcgctgactg cggcgcaactt cgccgcacat gcggcgatgt atcagtccgt 240
260 gagecgtcgg gctgctgcga ttcatgacca gttcgtggcc acccttgcca gcagcgccag 300
261 ctcgtagtgc gccactgaag tcgccaatgc ggcggcggcc agctaagcca ggaacagtcg 360
262 gcacgagaaa ccacgagaaa tagggacacg taatggtgga ttctggggcg ttaccaccgg 420
263 agatcaactc cgcgaggatg tacgccggcc cgggttcggc ctgctggtg gccgcggctc 480
264 agatgtggga cagcgtggcg agtgacctgt ttctggccgc gtcggcggtt cagtcggttg 540
265 tctggggtct gacggtgggg tcgtggatag gtctgctggc ggggtctgat gtggcgggcg 600
266 cctcgccgta tgtggcgtgg atgagcgtca ccgcggggca ggccgagctg accgccgcc 660
267 aggtccgggt tgcgtgcggc gcctacgaga cggcgatatg gctgacggtg ccccgccgg 720
268 tgatcgccga gaaccgtgct gaactgatga ttctgatagc gaccaacctc ttggggcaaa 780
269 acaccccggc gatcgcggtc aacgaggccg aatacggcga gatgtgggcc caagacgccg 840
270 ccgcgatggt tggtacgcc gcggcgacgg cgacggcgac ggcgacgtt ctgccgttcg 900
271 aggaggcgcc ggagatgacc agcgcggtg ggctcctcga gcaggccgcc gcggtcgagg 960
272 aggcctccga caccgccgcg gcgaaccagt tgatgaacaa tgtgccccag gcgctgcaac 1020
273 agctggccca gccacgcag ggcaccacgc cttcttccaa gctgggtggc ctgtggaaga 1080
274 cggctctgcc gcatcggtcg ccgatcagca acatggtgtc gatggccaac aaccacatgt 1140
275 cgatgaccaa ctcggtgtg tcgatgacca acacctgag ctcgatgttg aagggtttg 1200
276 ctccggcgcc gccgcccag gccgtgcaaa ccgcggcgca aaacggggtc cgggcgatga 1260
277 gctcgctggg cagctcgctg ggttcttcgg gtctggcgcg tggggtggcc gccacttg 1320
278 gtcggcgccg ctcggtcggt tcgttgctcg tgccgcaggc ctgggcccgc gccaccagg 1380
279 cagtcacccc ggcggcgcgg gcgctgccgc tgaccagcct gaccagcgcc gcggaaagag 1440
280 ggcccgggca gatgctggg gggctgccg tggggcagat gggcgccagg gccggtggtg 1500
281 ggctcagtg tgtgctgct gtccgcgcg gaccctatgt gatgccgat tctccggcg 1560
282 ccggctagga gagggggcg agactgtcgt tatttgacca gtgatcgcg gtctcggtgt 1620
283 ttccgcggcc ggctatgaca acagtcaatg tgcattgaaa gttacaggt ttaggtccag 1680
284 gttcaacaag gagacaggca acatggctc acgttttatg acggatccgc acgcgatgcg 1740

```

04,597,796B 6

<210> 10

<211> 596

<212> PRT

<213> Artificial Sequence

<223> Description of Artificial Sequence: fusion
protein TbH9-Ra35 (MTB59F)

<400> 10

> <220> Insert this
mandatory
numeric identifier
wherever <221>, <222>
or <223> is
shown
↓

The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

<210> 11
 <211> 2287
 <212> DNA
 <213> Mycobacterium tuberculosis
 <213> Artificial Sequence
 <220>
 <223> Description of Artificial Sequence: fusion
 protein Ra12-TbH9-Ra35 (MTB72F)

<213> can only have one response:

Artificial Sequence
or Unknown or
 Scientific name
 (Genus/species)

<210> 25
 <211> 851
 <212> DNA
 <213> Mycobacterium tuberculosis

<220>
 <223> MTB39 (TbH9) cDNA

<400> 25
 ctgcagggtg gcgtggatga gcgtcaccgc ggggcaggcc gagctgaccg ccgcccaggt 60
 ccgggttgct gcggcgccct acgagacggc gtatgggctg acggtgcccc cgccggtgat 120
 cgccgagaac cgtgctgaac tgatgattct gatagcgacc aacctcttgg ggcaaaacac 180
 cccggcgatc gcggtcaacg aggccgaata cggcgagatg tggggccaag acgcccggcg 240
 gatgtttggc tacgcccgcg cgacggcgac ggcgacggcg acgttgctgc cgttcgagga 300
 ggcgcgggag atgaccagcg cgggtgggct cctcgagcag gccgcgcgg tcgaggaggc 360
 ctccgacacc gccgcggcga accagttgat gaacaatgtg ccccgaggcg tgaaacagtt 420
 ggcccagccc acgcagggca ccacgccttc ttccaagctg ggtggcctgt ggaagacggt 480
 ctgcgcgcat cggtcgcca tcagcaacat ggtgtcgatg gccacaacc acatgtcgat 540
 gaccaactcg ggtgtgtcga tgaccaaacac cttgagctcg atgttgaaag gctttgctcc 600
 ggcggcgggc gcccaggccg tgcaaaccgc ggcgcaaaac ggggtccggg cgatgagctc 660
 gctgggcagc tcgctgggtt cttcggtgtc ggcgggtggg gtggccgcca acttgggtcg 720
 ggcggcctcg gtacggtatg gtcaccggga tggcggaata tatgcaggt ctggtcggcg 780
 gaacggtggt ccggcgtaag gtttaccgcc gttttctgga tgcggtgaac ttcgtcaacg 840
 gaaacagtta c 851

see
 item 9
 on Enon
 Summary
 Sheet

IMPORTANT
 ↳

Use of n or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/597,796B

DATE: 01/15/2002

TIME: 12:32:11

Input Set : A:\-90-5.app

Output Set: N:\CRF3\01152002\I597796B.raw

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
 L:132 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
 L:132 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
 L:132 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
 L:138 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:3
 L:138 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:3
 L:138 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
 L:421 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:508 M:280 W: Numeric Identifier already exists, Organism not replaced.
 L:535 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
 L:572 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
 L:580 M:258 W: Mandatory Feature missing, <220> FEATURE:
 L:788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:804 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:805 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17
 L:1082 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:25
 L:1082 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25
 L:1082 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:25
 L:1126 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:26
 L:1126 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26
 L:1126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26
 L:1181 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:27